

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaFAA4GaWRi: 704 aa
>SEQ ID NO:2
vs /tmp/fastaGAA5GaWRi library
searching /tmp/fastaGAA5GaWRi library

704 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 38, opt: 26, gap-pen: -12/ -2, width: 16
Scan time: 0.033

The best scores are:
gi|12583612|emb|CAC27329.1| neurolysin [Homo sapi (704) 4666

>>gi|12583612|emb|CAC27329.1| neurolysin [Homo sapiens]
(704 aa)

initn: 4666 initl: 4666 opt: 4666

Smith-Waterman score: 4666; 100.000% identity in 704 aa overlap (1-704:1-704)

SEQ	10	20	30	40	50	60
	MIARCLLAVRSLRRVGGSRILLRMTLGREVMSP	PLQAMSSYTVAGRNVL	RWDLSPEQIKTR			
gi 125	MIARCLLAVRSLRRVGGSRILLRMTLGREVMSP	PLQAMSSYTVAGRNVL	RWDLSPEQIKTR			
	10	20	30	40	50	60
SEQ	70	80	90	100	110	120
	TEELIVQTKQVYDAVGMLGIEEVTYENCLQALAD	VEVKYIVERTMLDFPQHVSSDKEVRA				
gi 125	TEELIVQTKQVYDAVGMLGIEEVTYENCLQALAD	VEVKYIVERTMLDFPQHVSSDKEVRA				
	70	80	90	100	110	120
SEQ	130	140	150	160	170	180
	ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCD	LGKIKPEARRYLEKSIKMGKRNLHL				
gi 125	ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCD	LGKIKPEARRYLEKSIKMGKRNLHL				
	130	140	150	160	170	180
SEQ	190	200	210	220	230	240
	PEQVQNEIKSMKKRMSEL	CIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK				
gi 125	PEQVQNEIKSMKKRMSEL	CIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK				
	190	200	210	220	230	240
SEQ	250	260	270	280	290	300
	ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE	ENTIILQQLPLRTKVAKLLGYSTHA				
gi 125	ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE	ENTIILQQLPLRTKVAKLLGYSTHA				
	250	260	270	280	290	300
SEQ	310	320	330	340	350	360
	DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA	REFILNLKKKECKDRGFEYDGGKINAWD				
gi 125	DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA	REFILNLKKKECKDRGFEYDGGKINAWD				
	310	320	330	340	350	360
	370	380	390	400	410	420

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SEQ      LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
          .....
gi|125   LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
          370      380      390      400      410      420

          430      440      450      460      470      480
SEQ      YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRRMMAVAALVVNFSQPV
          .....
gi|125   YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRRMMAVAALVVNFSQPV
          430      440      450      460      470      480

          490      500      510      520      530      540
SEQ      AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFAFSGTNNVETDFVEVPSQMLENWWVDVD
          .....
gi|125   AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFAFSGTNNVETDFVEVPSQMLENWWVDVD
          490      500      510      520      530      540

          550      560      570      580      590      600
SEQ      SLRRLSKHYKDGSPiADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
          .....
gi|125   SLRRLSKHYKDGSPiADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
          550      560      570      580      590      600

          610      620      630      640      650      660
SEQ      AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
          .....
gi|125   AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
          610      620      630      640      650      660

          670      680      690      700
SEQ      VGMKYRNILKPGGSLDGMDMLHNFLKREPQKAFLMSRGLHAP
          .....
gi|125   VGMKYRNILKPGGSLDGMDMLHNFLKREPQKAFLMSRGLHAP
          670      680      690      700
```

704 residues in 1 query sequences

704 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Fri Nov 1 15:59:40 2002 done: Fri Nov 1 15:59:41 2002

Scan time: 0.033 Display time: 0.700

Function used was FASTA